

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Wackett, Lawrence P.
Sadowsky, Michael J.
de Souza, Mervyn L.

(ii) TITLE OF INVENTION: An Isolated and Purified DNA Molecule
and Protein for the Degradation of Triazine Compounds

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
(B) STREET: P.O. Box 581415
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55458-1415

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mueting, Ann M.
(B) REGISTRATION NUMBER: 33,977
(C) REFERENCE/DOCKET NUMBER: 110.00230101

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 612-305-1217
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC TTCTTGAGCG CGGCCACAGC AGCCTTGATC ATGAAGGCGA GCATGGTGAC	60
CTTGACGCCG CTCTTTTCGT TCTCTTGTT GAACTGCACG CGAAAGGCTT CCAGGTCGGT	120
GATGTCCGCG TCGTCGTGGT TGGTGACGTG CGGGATGACC ACCCAGTTGC GGTGCAGGTT	180
TTTCGATGGC ATAATATCTG CGTTGCGACG TGTAACACAC TATTGGAGAC ATATCATGCA	240
AACGCTCAGC ATCCAGCACG GTACCCCTCGT CACGATGGAT CAGTACCGCA GAGTCCTTGG	300
GGATAGCTGG GTTCACGTGC AGGATGGACG GATCGTCGCG CTCGGAGTGC ACGCCGAGTC	360
GGTGCCTCCG CCAGCGGATC GGGTGATCGA TGCACGCCGC AAGGTCGTGT TACCCGGTTT	420
CATCAATGCC CACACCCATG TGAACCAGAT CCTCCTGCGC GGAGGGCCCT CGCACGGACG	480
TCAATTCTAT GACTGGCTGT TCAACGTTGT GTATCCGGGA CAAAAGGCGA TGAGACCGA	540
GGACGTAGCG GTGGCGGTGA GGTTGTATTG TGCGGAAGCT GTGCGCAGCG GGATTACGAC	600
GATCAACGAA AACGCCGATT CGGCCATCTA CCCAGGCAAC ATCGAGGCCG CGATGGCGGT	660
CTATGGTGAG GTGGGTGTGA GGGTCGTCTA CGCCCGCATG TTCTTGATC GGATGGACGG	720
GCGCATTCAA GGGTATGTGG ACGCCTTGAA GGCTCGCTCT CCCCAAGTCG AACTGTGCTC	780
GATCATGGAG GAAACGGCTG TGGCCAAAGA TCGGATCACA GCCCTGTCAG ATCAGTATCA	840
TGGCACGGCA GGAGGTCGTA TATCAGTTG GCCCGCTCCT GCCACTACCA CGGCGGTGAC	900
AGTTGAAGGA ATGCGATGGG CACAAGCCTT CGCCCGTGAT CGGGCGGTAA TGTGGACGCT	960
TCACATGGCG GAGAGCGATC ATGATGAGCG GATTGATGGG ATGAGTCCCG CCGAGTACAT	1020
GGAGTGTAC GGACTCTTGG ATGAGCGTCT GCAGGTCGCG CATTGCGTGT ACTTTGACCG	1080
GAAGGGATGTT CGGCTGCTGC ACCGCCACAA TGTGAAGGTC GCGTCGCAGG TTGTGAGCAA	1140
TGCCTACCTC GGCTCAGGGG TGGCCCCCGT GCCAGAGATG GTGGAGCGCG GCATGGCCGT	1200

GGGCATTGGA ACAGATAACG GGAATAGTAA TGACTCCGCA AACATGATCG GAGACATGAA 1260
 GTTTATGGCC CATATTCACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA 1320
 GATTCTTGAA ATGGCGACGA TCGATGGGC GCGTTCGTTG GGAATGGACC ACGAGATTGG 1380
 TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG 1440
 ACTCTCACAT CATTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC 1500
 TGTCTTGATT GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA 1560
 ACGTGAGTTG GCGTTCCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGC 1620
 GAACATGGTG GCTAACCCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC 1680
 GCCGCCCCCTT GAGGAAATCG CTGCCATCTT GGCGCGGCTC GGATTGGGG GCGGACATGA 1740
 CCTTGATGGA TACAGAATTG CCATGAATGC GGCACCTCCG TCCTTCGCTC GTGTGGAATC 1800
 GTTGGTAGGT GAGGGTCGAC TGCGGGCGCC AGCTTCCGA AGAGGTGAAA GGCCCGAG 1858

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
 1 5 10 15

Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
 20 25 30

Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp
 35 40 45

Arg Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
 50 55 60

Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
 65 70 75 80

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95
 Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110
 Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125
 Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140
 Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160
 Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175
 Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190
 Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205
 Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220
 Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240
 Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255
 Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270
 Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285
 His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300
 Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320
 Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Ala Asn
 325 330 335
 Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350

Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
355 360 365

Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
370 375 380

Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Leu
385 390 395 400

Arg Arg Leu Ser His His Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr
405 410 415

Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met Glu
420 425 430

Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu
435 440 445

Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn Met
450 455 460

Val Ala Asn Pro Ala Trp Arg Ser Leu
465 470